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Reviewer: Anne Corrigan

Timestamp: [year=2007; month=12; day=20; hr=11; min=45; sec=45; ms=947;
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Application No: 10578615 Version No: 1.0

Input Set:**Output Set:**

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Finished: 2007-12-20 11:22:51.814
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 2 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
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W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

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Error code	Error Description
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<110> Tohata, Masatoshi
Sawada, Kazuhisa
Ozaki, Katsuya
Sekiguchi, Junichi

<120> RECOMBINANT MICROORGANISM

<130> 288704US0PCT

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<150> PCT/JP04/16890

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<150> JP 2003-379114

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<170> PatentIn version 3.3

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Phe Pro Ala Ala Leu Ala Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe	
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aaa cat tta tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc	737
Lys His Leu Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly	
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Ala Leu Gln Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln	
60 65 70	
cat gga gaa aaa att caa tta cgt gga atg agt aca cac gga tta cag	833
His Gly Glu Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln	
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Trp Phe Pro Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn	
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gat tgg gat tcc aat atg att cgt ctt gct atg tat gta ggt gaa aat	929
Asp Trp Asp Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn	
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Gly Tyr Ala Thr Asn Pro Glu Leu Ile Lys Gln Arg Val Ile Asp Gly	
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Val His Ala Pro Gly Asp Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys	
155 160 165	
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185 190 195	
ggg att ccg aat aac gaa gaa ggt tgg aaa gcg gta aaa gaa tat gct	1217
Gly Ile Pro Asn Asn Glu Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala	
200 205 210 215	

gat cca att gta gaa atg tta cgt aaa agc ggt aat gca gat gac aac	1265
Asp Pro Ile Val Glu Met Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn	
220 225 230	
att atc att gtt ggt agt cca aac tgg agt cag cgt ccg gac tta gca	1313
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235 240 245	
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Ala Asp Asn Pro Ile Asp Asp His His Thr Met Tyr Thr Val His Phe	
250 255 260	
tac act ggt tca cat gct gct tca act gaa agc tat ccg tct gaa act	1409
Tyr Thr Gly Ser His Ala Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr	
265 270 275	
cct aac tct gaa aga gga aac gta atg agt aac act cgt tat gcg tta	1457
Pro Asn Ser Glu Arg Gly Asn Val Met Ser Asn Thr Arg Tyr Ala Leu	
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Glu Asn Gly Val Ala Val Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala	
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Ser Gly Asp Gly Gly Pro Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu	
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Phe Leu Asn Glu Asn Asn Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn	
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Lys Asn Glu Val Ser Gly Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser	
345 350 355	
aac gca acc aat ctt gac cca ggt cca gat cat gtg tgg gca cca gaa	1697
Asn Ala Thr Asn Leu Asp Pro Gly Pro Asp His Val Trp Ala Pro Glu	
360 365 370 375	
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380 385 390	
aac tat gag cca atc gac cgt aca aaa tac acg aaa gta ctt tgg gac	1793
Asn Tyr Glu Pro Ile Asp Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp	
395 400 405	
ttt aat gat gga acg aag caa gga ttt gga gtg aat tcg gat tct cca	1841
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410 415 420	
aat aaa gaa ctt att gca gtt gat aat gaa aac aac act ttg aaa gtt	1889
Asn Lys Glu Leu Ile Ala Val Asp Asn Glu Asn Asn Thr Leu Lys Val	
425 430 435	
tcg gga tta gat gta agt aac gat gtt tca gat ggc aac ttc tgg gct	1937

Ser Gly Leu Asp Val	Ser Asn Asp Val	Ser Asp Gly Asn Phe Trp Ala	
440	445	450	455
aat gct cgt ctt tct gcc aac ggt tgg gga aaa agt gtt gat att tta			1985
Asn Ala Arg Leu Ser Ala Asn Gly Trp Gly Lys Ser Val Asp Ile Leu			
460	465	470	
ggg gct gag aag ctt aca atg gat gtt att gtt gat gaa cca acg acg			2033
Gly Ala Glu Lys Leu Thr Met Asp Val Ile Val Asp Glu Pro Thr Thr			
475	480	485	
gta gct att gcg gcg att cca caa agt agt aaa agt gga tgg gca aat			2081
Val Ala Ile Ala Ala Ile Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn			
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cca gag cgt gct gtt cga gtg aac gcg gaa gat ttt gtc cag caa acg			2129
Pro Glu Arg Ala Val Arg Val Asn Ala Glu Asp Phe Val Gln Gln Thr			
505	510	515	
gac ggt aag tat aaa gct gga tta aca att aca gga gaa gat gct cct			2177
Asp Gly Lys Tyr Lys Ala Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro			
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aac cta aaa aat atc gct ttt cat gaa gaa gat aac aat atg aac aac			2225
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570	575	580	
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Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe Glu Asp Gly Thr Arg			
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caa ggt tgg gac tgg gct gga gag tct ggt gtg aaa aca gct tta aca			2417
Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val Lys Thr Ala Leu Thr			
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att gaa gaa gca aac ggt tct aac gcg tta tca tgg gaa ttt gga tat			2465
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620	625	630	
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Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp			
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ttc tgg aaa tct gac ttg gtt cgc ggt gag aat gat tat gta gct ttt			2561
Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn Asp Tyr Val Ala Phe			
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gat ttc tat cta gat cca gtt cgt gca aca gaa ggc gca atg aat atc			2609
Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu Gly Ala Met Asn Ile			

665	670	675	
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Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu Glu Ala Asn Gln Val			
700	705	710	
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Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn Val Arg Asp Ile Thr			
715	720	725	
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730	735	740	
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745	750	755	
ttt gag ggg gct gct act act gag ccg gtt gaa cca gag cca gtt gat			2897
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760	765	770	775
cct ggc gaa gag acg cca cct gtc gat gag aag gaa gcg aaa aaa gaa			2945
Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys Glu Ala Lys Lys Glu			
780	785	790	
caa aaa gaa gca gag aaa gaa gag aaa gaa gca gta aaa gaa gaa aag			2993
Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala Val Lys Glu Glu Lys			
795	800	805	
aaa gaa gct aaa gaa gaa aag aaa gca gtc aaa aat gag gct aag aaa			3041
Lys Glu Ala Lys Glu Glu Lys Lys Ala Val Lys Asn Glu Ala Lys Lys			
810	815	820	
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30

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val
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Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly
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Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly
 65 70 75 80

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn
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Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu
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Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile
 115 120 125

Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met
 130 135 140

Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp
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Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp
 195 200 205

Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys
 210 215 220

Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
 225 230 235 240

Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
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Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr
260 265 270

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305 310 315 320

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450 455 460

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485 490 495

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500 505 510

Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala Gly Leu Thr
515 520 525

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